

SEQUENCE LISTING

<110> Yaar, Liora
Alroy, Iris
Reiss, Yuval
Taglicht, Daniel N.

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METHODS

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Gln	Ser	Glu	Ala	Glu	Leu	Glu	Leu	Lys	Glu	Gly	Asp	Ile	Val	Phe	Val
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 caggtaatgc gccgagttga tcataattgg gcagaaggac gaattggcca gaccatcgga 1020
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 tcgggcttcc aaatacgaa tctcatattt ctcttttcaa aaaagaaacc gttttgtact 2940
 ctccaatcg aatgggcagc tcgcccgtt acttttttatacaatgcctt atcaaaatag 3000
 gctagccatg taagacttag ggaacagttt cttaaacccctt agcgattttt tagctagaga 3060
 aataatctaa ccgatccttgc tgccctctac aaagtttattt gtaatatacg atactcagta 3120
 ataaaaaaaaaaaaaaa 3149

<210> 11
 <211> 838
 <212> PRT
 <213> Drosophila melanogaster

<400> 11
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 20 25 30
 Cys Arg Lys Cys Leu Gln Asp Ile Val Ala Ser Gln His Lys Leu Arg
 35 40 45
 Cys Pro Glu Cys Arg Ile Leu Val Ser Cys Lys Ile Asp Glu Leu Pro
 50 55 60
 Pro Asn Val Leu Leu Met Arg Ile Leu Glu Gly Met Lys Gln Asn Ala
 65 70 75 80
 Ala Ala Gly Lys Gly Glu Glu Lys Gly Glu Glu Thr Glu Thr Gln Pro
 85 90 95
 Glu Arg Ala Lys Pro Gln Pro Pro Ala Glu Ser Val Ala Pro Pro Asp
 100 105 110
 Asn Gln Leu Leu Gln Leu Gln Ser His Gln Gln Ser His Gln Pro Ala
 115 120 125
 Arg His Lys Gln Arg Arg Phe Leu Leu Pro His Ala Tyr Ala Leu Phe
 130 135 140
 Asp Phe Ala Ser Gly Glu Ala Thr Asp Leu Lys Phe Lys Lys Gly Asp
 145 150 155 160
 Leu Ile Leu Ile Lys His Arg Ile Asp Asn Asn Trp Phe Val Gly Gln
 165 170 175
 Ala Asn Gly Gln Glu Gly Thr Phe Pro Ile Asn Tyr Val Lys Val Ser
 180 185 190
 Val Pro Leu Pro Met Pro Gln Cys Ile Ala Met Tyr Asp Phe Lys Met
 195 200 205

Gly Pro Asn Asp Glu Glu Gly Cys Leu Glu Phe Lys Lys Ser Thr Val
 210 215 220
 Ile Gln Val Met Arg Arg Val Asp His Asn Trp Ala Glu Gly Arg Ile
 225 230 235 240
 Gly Gln Thr Ile Gly Ile Phe Pro Ile Ala Phe Val Glu Leu Asn Ala
 245 250 255
 Ala Ala Lys Lys Leu Leu Asp Ser Gly Leu His Thr His Pro Phe Cys
 260 265 270
 His Pro Pro Lys Gln Gln Gly Gln Arg Ala Leu Pro Pro Val Pro Val
 275 280 285
 Ile Asp Pro Thr Val Val Thr Glu Ser Ser Ser Gly Ser Ser Asn Ser
 290 295 300
 Thr Pro Gly Ser Ser Asn Ser Ser Ser Thr Ser Ser Ser Asn Asn Cys
 305 310 315 320
 Ser Pro Asn His Gln Ile Ser Leu Pro Asn Thr Pro Gln His Val Val
 325 330 335
 Ala Ser Gly Ser Ala Ser Val Arg Phe Arg Asp Lys Gly Ala Lys Glu
 340 345 350
 Lys Arg His Ser Leu Asn Ala Leu Leu Gly Gly Gly Ala Pro Leu Ser
 355 360 365
 Leu Leu Gln Thr Asn Arg His Ser Ala Glu Ile Leu Ser Leu Pro His
 370 375 380
 Glu Leu Ser Arg Leu Glu Val Ser Ser Ser Thr Ala Leu Lys Pro Thr
 385 390 395 400
 Ser Ala Pro Gln Thr Ser Arg Val Leu Lys Thr Thr Val Gln Gln Gln
 405 410 415
 Met Gln Pro Asn Leu Pro Trp Gly Tyr Leu Ala Leu Phe Pro Tyr Lys
 420 425 430
 Pro Arg Gln Thr Asp Glu Leu Glu Leu Lys Lys Gly Cys Val Tyr Ile
 435 440 445
 Val Thr Glu Arg Cys Val Asp Gly Trp Phe Lys Gly Lys Asn Trp Leu
 450 455 460
 Asp Ile Thr Gly Val Phe Pro Gly Asn Tyr Leu Thr Pro Leu Arg Ala
 465 470 475 480
 Arg Asp Gln Gln Gln Leu Met His Gln Trp Lys Tyr Val Pro Gln Asn
 485 490 495
 Ala Asp Ala Gln Met Ala Gln Val Gln Gln His Pro Val Ala Pro Asp
 500 505 510
 Val Arg Leu Asn Asn Met Leu Ser Met Gln Pro Pro Asp Leu Pro Pro
 515 520 525
 Arg Gln Gln Gln Ala Thr Ala Thr Thr Thr Ser Cys Ser Val Trp Ser
 530 535 540
 Lys Pro Val Glu Ala Leu Phe Ser Arg Lys Ser Glu Pro Lys Pro Glu
 545 550 555 560
 Thr Ala Thr Ala Ser Thr Thr Ser Ser Ser Ser Gly Ala Val Gly
 565 570 575
 Leu Met Arg Arg Leu Thr His Met Lys Thr Arg Ser Lys Ser Pro Gly
 580 585 590
 Ala Ser Leu Gln Gln Val Pro Lys Glu Ala Ile Ser Thr Asn Val Glu
 595 600 605
 Phe Thr Thr Asn Pro Ser Ala Lys Leu His Pro Val His Val Arg Ser
 610 615 620
 Gly Ser Cys Pro Ser Gln Leu Gln His Ser Gln Pro Leu Asn Glu Thr
 625 630 635 640
 Pro Ala Ala Lys Thr Ala Ala Gln Gln Gln Phe Leu Pro Lys Gln
 645 650 655
 Leu Pro Ser Ala Ser Thr Asn Ser Val Ser Tyr Gly Ser Gln Arg Val
 660 665 670

Lys Gly Ser Lys Glu Arg Pro His Leu Ile Cys Ala Arg Gln Ser Leu
 675 680 685
 Asp Ala Ala Thr Phe Arg Ser Met Tyr Asn Asn Ala Ala Ser Pro Pro
 690 695 700
 Pro Pro Thr Thr Ser Val Ala Pro Ala Val Tyr Ala Gly Gly Gln Gln
 705 710 715 720
 Gln Val Ile Pro Gly Gly Ala Gln Ser Gln Leu His Ala Asn Met
 725 730 735
 Ile Ile Ala Pro Ser His Arg Lys Ser His Ser Leu Asp Ala Ser His
 740 745 750
 Val Leu Ser Pro Ser Ser Asn Met Ile Thr Glu Ala Ala Ile Lys Ala
 755 760 765
 Ser Ala Thr Thr Lys Ser Pro Tyr Cys Thr Arg Glu Ser Arg Phe Arg
 770 775 780
 Cys Ile Val Pro Tyr Pro Pro Asn Ser Asp Ile Glu Leu Glu Leu His
 785 790 795 800
 Leu Gly Asp Ile Ile Tyr Val Gln Arg Lys Gln Lys Asn Gly Trp Tyr
 805 810 815
 Lys Gly Thr His Ala Arg Thr His Lys Thr Gly Leu Phe Pro Ala Ser
 820 825 830
 Phe Val Glu Pro Asp Cys
 835

<210> 12
 <211> 18
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 <213> Artificial Sequence

<220>
 <223> primer

<400> 12
 cttgccttgc cagcatac

18

<210> 13
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer

<400> 13
 ctgccagcat tccttcag

18

<210> 14
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> target sequence

<400> 14
 aacagaggcc ttggaaacct g

21

<210> 15
 <211> 21

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<212> DNA
<213> Artificial Sequence

<220>
<223> siRNA

<400> 15
ttcagaggcc uuggaaaccu g 21

<210> 16
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> siRNA

<400> 16
ttcagguuuc caaggccucu g 21

<210> 17
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> target sequence

<400> 17
aaagagcctg gagacacctaa a 21

<210> 18
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> siRNA

<400> 18
tttagagccug gagaccuuua a 21

<210> 19
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> siRNA

<400> 19
ttuuuaaggu cuccaggcuc u 21

<210> 20
<211> 21
<212> DNA
<213> Artificial Sequence

<220>

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<223> target sequence

<400> 20
aaggatttgt atgtgactct g 21

<210> 21
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> siRNA

<400> 21
ttggauuggu augugacucu g 21

<210> 22
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> siRNA

<400> 22
ttcagaguca cauaccaauc c 21

<210> 23
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> target sequence

<400> 23
aagctggatt atctcctgtt g 21

<210> 24
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> siRNA

<400> 24
ttgcuggauu aucuccuguu g 21

<210> 25
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> siRNA

<400> 25
ttcaacagga gauaauccag c 21

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<210> 26
<211> 41
<212> PRT
<213> Artificial Sequence

<220>
<223> RING domain

<400> 26
Cys Pro Val Cys Leu Glu Arg Leu Asp Ala Ser Ala Lys Val Leu Pro
1 5 10 15
Cys Gln His Thr Phe Cys Lys Arg Cys Leu Leu Gly Ile Val Gly Ser
20 25 30
Arg Asn Glu Leu Arg Cys Pro Glu Cys
35 40

<210> 27
<211> 56
<212> PRT
<213> Artificial Sequence

<220>
<223> SH3 domain

<400> 27
Pro Cys Ala Lys Ala Leu Tyr Asn Tyr Glu Gly Lys Glu Pro Gly Asp
1 5 10 15
Leu Lys Phe Ser Lys Gly Asp Ile Ile Ile Leu Arg Arg Gln Val Asp
20 25 30
Glu Asn Trp Tyr His Gly Glu Val Asn Gly Ile His Gly Phe Phe Pro
35 40 45
Thr Asn Phe Val Gln Ile Ile Lys
50 55

<210> 28
<211> 60
<212> PRT
<213> Artificial Sequence

<220>
<223> SH3 domain

<400> 28
Pro Gln Cys Lys Ala Leu Tyr Asp Phe Glu Val Lys Asp Lys Glu Ala
1 5 10 15
Asp Lys Asp Cys Leu Pro Phe Ala Lys Asp Asp Val Leu Thr Val Ile
20 25 30
Arg Arg Val Asp Glu Asn Trp Ala Glu Gly Met Leu Ala Asp Lys Ile
35 40 45
Gly Ile Phe Pro Ile Ser Tyr Val Glu Phe Asn Ser
50 55 60

<210> 29
<211> 58
<212> PRT
<213> Artificial Sequence

<220>
<223> SH3 domain

<400> 29
Ser Val Tyr Val Ala Ile Tyr Pro Tyr Thr Pro Arg Lys Glu Asp Glu
1 5 10 15
Leu Glu Leu Arg Lys Gly Glu Met Phe Leu Val Phe Glu Arg Cys Gln
20 25 30
Asp Gly Trp Phe Lys Gly Thr Ser Met His Thr Ser Lys Ile Gly Val
35 40 45
Phe Pro Gly Asn Tyr Val Ala Pro Val Thr
50 55

<210> 30
<211> 57
<212> PRT
<213> Artificial Sequence

<220>
<223> SH3 domain

<400> 30
Glu Arg His Arg Val Val Val Ser Tyr Pro Pro Gln Ser Glu Ala Glu
1 5 10 15
Leu Glu Leu Lys Glu Gly Asp Ile Val Phe Val His Lys Lys Arg Glu
20 25 30
Asp Gly Trp Phe Lys Gly Thr Leu Gln Arg Asn Gly Lys Thr Gly Leu
35 40 45
Phe Pro Gly Ser Phe Val Glu Asn Ile
50 55

<210> 31
<211> 121
<212> DNA
<213> Artificial Sequence

<220>
<223> RING domain

<400> 31
tgtccgggtgt gtcttagagcg ctttgatgct tctgcgaagg tcttgccttg ccagcatacg 60
tttgcaagc gatgttgct ggggatcgta gtttcgaa atgaactcag atgtcccgag 120
t 121

<210> 32
<211> 165
<212> DNA
<213> Artificial Sequence

<220>
<223> SH3 domain

<400> 32
ccatgtgcc aagcgttata caactatgaa ggaaaagagc ctggagacct taaattcagc 60
aaaggcgaca tcattttt gcaagacaa gtggatgaaa attggatcca tggggaaatgc 120
aatggaatcc atggctttt cccccaccaac ttgtgcaga ttatt 165

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<210> 33
<211> 177
<212> DNA
<213> Artificial Sequence

<220>
<223> SH3 domain

<400> 33
cctcagtgc aagcacttta tgactttgaa gtgaaagaca aggaaggcaga caaagattgc 60
cttcatttg caaaggatga tggatccgaa gatgtggatga aaactggct 120
gaaggaatgc tggcagacaa aataggaata tttccaattt catatgttga gtttaac 177

<210> 34
<211> 171
<212> DNA
<213> Artificial Sequence

<220>
<223> SH3 domain

<400> 34
agtgtgtatg ttgctatata tccatacact cctcgaaag agatgaact agagctgaga 60
aaaggggaga tggatgttgc tgccaggatg gctggttcaa agggacatcc 120
atgcataccca gcaagatagg gttttccct ggcaattatg tggcaccagt c 171

<210> 35
<211> 169
<212> DNA
<213> Artificial Sequence

<220>
<223> SH3 domain

<400> 35
gaaaggcaca gggtggtgggt ttcctatcct cctcagagtg aggcaact tgaactaaa 60
gaaggagata ttgtgttgt tcataaaaaaa cgagaggatg gctggttcaa aggcacatta 120
caacgtaatg gaaaactgg cttttccca ggaagcttg tggaaaaca 169

<210> 36
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> target sequence

<400> 36
aagtccaaag gttccggaga c 21

<210> 37
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> motif

<220>

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<221> VARIANT
<222> 2
<223> Xaa = Thr or Ser

<400> 37
Pro Xaa Ala Pro
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<210> 38
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> motif

<400> 38
Pro Phe Arg Asp Tyr
1 5

<210> 39
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> motif

<400> 39
Arg Pro Glu Pro Thr Ala Pro
1 5

<210> 40
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> motif

<400> 40
Arg Gln Gly Pro Lys Glu Pro
1 5

<210> 41
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> motif

<400> 41
Arg Gln Gly Pro Lys Glu Pro Phe Arg
1 5

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<210> 42
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> motif

<400> 42
Arg Pro Glu Pro Thr Ala Pro Glu Glu
 1           5

<210> 43
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> motif

<400> 43
Arg Pro Leu Pro Val Ala Pro
 1           5

<210> 44
<211> 53
<212> DNA
<213> Artificial Sequence

<220>
<223> scrambled human POSH oligonucleotide

<400> 44
cacacactgc cgtcaactgt tcaagagaca gttgacggca gtgtgtgttt ttt      53

<210> 45
<211> 61
<212> DNA
<213> Artificial Sequence

<220>
<223> scrambled human POSH oligonucleotide

<400> 45
aattaaaaaaaa cacacactgc cgtcaactgt ctcttgaaca gttgacggca gtgtgtggc 60
C           61

<210> 46
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide encoding RNAi against human POSH

<400> 46

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aacagaggcc ttggaaacct ggaagcttgc aggtttccaa ggccctctgtt 50

<210> 47
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide encoding RNAi against human POSH

<400> 47
gatcaacaga ggccttgaa acctgcaagc ttccaggttt ccaaggcctc tgtt 54

<210> 48
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 48
ggcccactag tcaaggtcgg gcaggaaga 29

<210> 49
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 49
gccgaattca aaaaggatcc ggcgatatcc ggtgtttcgt cctttcca 48

<210> 50
<211> 836
<212> PRT
<213> Artificial Sequence

<220>
<223> POSH fragment

<400> 50
Arg Thr Leu Val Gly Ser Gly Val Glu Glu Leu Pro Ser Asn Ile Leu
1 5 10 15
Leu Val Arg Leu Leu Asp Gly Ile Lys Gln Arg Pro Trp Lys Pro Gly
20 25 30
Pro Gly Gly Ser Gly Thr Asn Cys Thr Asn Ala Leu Arg Ser Gln
35 40 45
Ser Ser Thr Val Ala Asn Cys Ser Ser Lys Asp Leu Gln Ser Ser Gln
50 55 60
Gly Gly Gln Gln Pro Arg Val Gln Ser Trp Ser Pro Pro Val Arg Gly
65 70 75 80
Ile Pro Gln Leu Pro Cys Ala Lys Ala Leu Tyr Asn Tyr Glu Gly Lys
85 90 95
Glu Pro Gly Asp Leu Lys Phe Ser Lys Gly Asp Ile Ile Ile Leu Arg
100 105 110

Arg Gln Val Asp Glu Asn Trp Tyr His Gly Glu Val Asn Gly Ile His
 115 120 125
 Gly Phe Phe Pro Thr Asn Phe Val Gln Ile Ile Lys Pro Leu Pro Gln
 130 135 140
 Pro Pro Pro Gln Cys Lys Ala Leu Tyr Asp Phe Glu Val Lys Asp Lys
 145 150 155 160
 Glu Ala Asp Lys Asp Cys Leu Pro Phe Ala Lys Asp Asp Val Leu Thr
 165 170 175
 Val Ile Arg Arg Val Asp Glu Asn Trp Ala Glu Gly Met Leu Ala Asp
 180 185 190
 Lys Ile Gly Ile Phe Pro Ile Ser Tyr Val Glu Phe Asn Ser Ala Ala
 195 200 205
 Lys Gln Leu Ile Glu Trp Asp Lys Pro Pro Val Pro Gly Val Asp Ala
 210 215 220
 Gly Glu Cys Ser Ser Ala Ala Gln Ser Ser Thr Ala Pro Lys His
 225 230 235 240
 Ser Asp Thr Lys Lys Asn Thr Lys Lys Arg His Ser Phe Thr Ser Leu
 245 250 255
 Thr Met Ala Asn Lys Ser Ser Gln Ala Ser Gln Asn Arg His Ser Met
 260 265 270
 Glu Ile Ser Pro Pro Val Leu Ile Ser Ser Ser Asn Pro Thr Ala Ala
 275 280 285
 Ala Arg Ile Ser Glu Leu Ser Gly Leu Ser Cys Ser Ala Pro Ser Gln
 290 295 300
 Val His Ile Ser Thr Thr Gly Leu Ile Val Thr Pro Pro Pro Ser Ser
 305 310 315 320
 Pro Val Thr Thr Gly Pro Ser Phe Thr Phe Pro Ser Asp Val Pro Tyr
 325 330 335
 Gln Ala Ala Leu Gly Thr Leu Asn Pro Pro Leu Pro Pro Pro Leu
 340 345 350
 Leu Ala Ala Thr Val Leu Ala Ser Thr Pro Pro Gly Ala Thr Ala Ala
 355 360 365
 Ala Ala Ala Gly Met Gly Pro Arg Pro Met Ala Gly Ser Thr Asp
 370 375 380
 Gln Ile Ala His Leu Arg Pro Gln Thr Arg Pro Ser Val Tyr Val Ala
 385 390 395 400
 Ile Tyr Pro Tyr Thr Pro Arg Lys Glu Asp Glu Leu Glu Leu Arg Lys
 405 410 415
 Gly Glu Met Phe Leu Val Phe Glu Arg Cys Gln Asp Gly Trp Phe Lys
 420 425 430
 Gly Thr Ser Met His Thr Ser Lys Ile Gly Val Phe Pro Gly Asn Tyr
 435 440 445
 Val Ala Pro Val Thr Arg Ala Val Thr Asn Ala Ser Gln Ala Lys Val
 450 455 460
 Pro Met Ser Thr Ala Gly Gln Thr Ser Arg Gly Val Thr Met Val Ser
 465 470 475 480
 Pro Ser Thr Ala Gly Gly Pro Ala Gln Lys Leu Gln Gly Asn Gly Val
 485 490 495
 Ala Gly Ser Pro Ser Val Val Pro Ala Ala Val Val Ser Ala Ala His
 500 505 510
 Ile Gln Thr Ser Pro Gln Ala Lys Val Leu Leu His Met Thr Gly Gln
 515 520 525
 Met Thr Val Asn Gln Ala Arg Asn Ala Val Arg Thr Val Ala Ala His
 530 535 540
 Asn Gln Glu Arg Pro Thr Ala Ala Val Thr Pro Ile Gln Val Gln Asn
 545 550 555 560
 Ala Ala Gly Leu Ser Pro Ala Ser Val Gly Leu Ser His His Ser Leu
 565 570 575

Ala Ser Pro Gln Pro Ala Pro Leu Met Pro Gly Ser Ala Thr His Thr
 580 585 590
 Ala Ala Ile Ser Ile Ser Arg Ala Ser Ala Pro Leu Ala Cys Ala Ala
 595 600 605
 Ala Ala Pro Leu Thr Ser Pro Ser Ile Thr Ser Ala Ser Leu Glu Ala
 610 615 620
 Glu Pro Ser Gly Arg Ile Val Thr Val Leu Pro Gly Leu Pro Thr Ser
 625 630 635 640
 Pro Asp Ser Ala Ser Ser Ala Cys Gly Asn Ser Ser Ala Thr Lys Pro
 645 650 655
 Asp Lys Asp Ser Lys Lys Glu Lys Lys Gly Leu Leu Lys Leu Leu Ser
 660 665 670
 Gly Ala Ser Thr Lys Arg Lys Pro Arg Val Ser Pro Pro Ala Ser Pro
 675 680 685
 Thr Leu Glu Val Glu Leu Gly Ser Ala Glu Leu Pro Leu Gln Gly Ala
 690 695 700
 Val Gly Pro Glu Leu Pro Pro Gly Gly His Gly Arg Ala Gly Ser
 705 710 715 720
 Cys Pro Val Asp Gly Asp Gly Pro Val Thr Thr Ala Val Ala Gly Ala
 725 730 735
 Ala Leu Ala Gln Asp Ala Phe His Arg Lys Ala Ser Ser Leu Asp Ser
 740 745 750
 Ala Val Pro Ile Ala Pro Pro Arg Gln Ala Cys Ser Ser Leu Gly
 755 760 765
 Pro Val Leu Asn Glu Ser Arg Pro Val Val Cys Glu Arg His Arg Val
 770 775 780
 Val Val Ser Tyr Pro Pro Gln Ser Glu Ala Glu Leu Glu Leu Lys Glu
 785 790 795 800
 Gly Asp Ile Val Phe Val His Lys Lys Arg Glu Asp Gly Trp Phe Lys
 805 810 815
 Gly Thr Leu Gln Arg Asn Gly Lys Thr Gly Leu Phe Pro Gly Ser Phe
 820 825 830
 Val Glu Asn Ile
 835

<210> 51
 <211> 1502
 <212> DNA
 <213> Homo sapiens

<400> 51
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 taggagcgca gcggagcccc gacaccgccc ccgcccgcatt ggagtccgag accgaaccgg 120
 agcccgtaac gctcctggtg aagagccccca accagcgccca ccgcgcacttg gagctgagtg 180
 gcgaccgcgg ctggagtgtg ggccacacctt aaggcccacctt gagccgcgtc taccggcggc 240
 gtccgcgtcc agaggaccag aggttaattt attctggaa gctgttggtg gatcaccaat 300
 gtctcaggga cttgcttcca aaggaaaaac ggcatgtttt gcatctggtg tgcaatgtga 360
 agagtccttc aaaaatgcca gaaatcaacg ccaaggtggc tgaatccaca gaggagcctg 420
 ctggttctaa tcggggacag tatcctgagg attcctcaag tgatggtttta aggccaaagg 480
 aagttcttcg gaacctttct tcccctggat gggaaaacat ctcaaggcat cacgttgggt 540
 ggttccatt tagaccgagg ccgggttcaga acttcccaa tgatggctt cctcctgacg 600
 ttgttaatca ggaccccaac aataacttac aggaaggcac tgatcctgaa actgaagacc 660
 ccaaccaccc cccctccagac agggatgtac tagatggcga gcagaccgc ccctccttta 720
 tgagcacagc atggcttgc ttcaagactt tctttgcctc tcttcttcca gaaggcccc 780
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 <213> Homo sapiens

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<400> 53

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<210> 54

<211> 1878

<212> DNA

<213> Homo sapiens

<400> 54

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<211> 1864  
<212> DNA  
<213> Homo sapiens
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<210> 56  
<211> 1871  
<212> DNA  
<213> Homo sapiens
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<210> 57
 <211> 1865
 <212> DNA
 <213> Homo sapiens

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<212> DNA  
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<211> 1860  
<212> DNA  
<213> Homo sapiens
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 cctgctccag cccctattca caaccagtt ccagctgaaa accagcctgc caatcagaat 780
 gctgctctc aagtgggtgt taatcctgga gccaatcaaa atttgcggat gaatgcacaa 840
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 ctcctccag acaggatgt actagatggc gagcagacca gcccctcct tatgagcaca 1200
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 gcaaactgat ggtgttgtg ctgtagctgt tggaggctt gacaggaatg gactggatca 1320
 cctgactcca gctagattgc ctccctgga catggcaatg atgagttttt aaaaaacagt 1380
 gtggatgatg atatgccccatgtt gtgagcaagc aaaagcagaa acgtgaagcc gtgataaaaa 1440
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 actctatgtt gtttaataag cactgtacgt agaaggcctt aggtgttgca tgtctatgt 1560
 tgaggaactt ttccaaatgt gtgtgtctgc atgtgtgtt gtacatagaa gtcatagatg 1620
 cagaagtggg tctgctggta agatttgatt cctgtggaa tttttttttt acactaagtg 1680
 tactacttta tataatcaat gaaattgcta gacatgtttt agcaggactt ttcttagaaaa 1740
 gacttatgtt taattgcttt taaaatgca gtgcttact taaaactaag gggactttg 1800
 cgaggtgaa aaccttgcg gggtttctg ttcaataaag ttactatg aatgaccctg 1860

<210> 60
 <211> 1884
 <212> DNA
 <213> Homo sapiens

<400> 60
 gacgtgaacg gtcgttgcag agattgcggg cggctgagac gcccctgcc tggcacctag 60
 gagcgcagcg gagcccccac accgcgcggc cgcgcattggat gtcgcggacc gaacccgagc 120
 ccgtcacgct cctgggtgaag agccccaacc agcgcaccgc cgacttggag ctgagtggcg 180
 accgcggctg gagtgtggc cacctcaagg cccacctgag cgcgtctac cccgagcgctc 240
 cgcgtccaga ggaccagagg ttaattttt ctggaaagct gttgtggat caccaatgtc 300
 tcagggactt gcttccaaag cagaaaaac ggcattgtttt gcatctggtg tgcaatgtga 360
 agagtccctc aaaaatgcca gaaatcaacg ccaaggtggc tgaatccaca gaggagcctg 420
 ctgggtctaa tcggggacag tattctgagg attcctcaag tgatggttt agccaaagg 480
 aagttcttcg gaaccttctt tccctggat gggaaaacat ctcaaggcct gaagctgccc 540
 agcaggcatt ccaaggcctg ggtcctgggt tctccggta cacaccctat ggggtggcttc 600
 agtttctcg gttccagcag atatatgcac gacagtacta catgcaatat ttagcagcca 660
 ctgctgcatac aggggtttt gttccaccac caagtgcaca agagatactt gtggctctg 720
 cacctgtcc agcccttatt cacaaccagt ttccagctga aaaccagcct gccaatcaga 780
 atgctgtcc tcaagtgggtt gttatcctg gagccaatca aaatttgcgg atgaatgcac 840
 aaggtggccc tattgtggaa gaagatgtg aaataaatcg agattggttt gattggacct 900
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 gattcctcat ggtcatgggg gccaccgtt ttatgtacct gcatcacgtt ggggtggttc 1020
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 atcaggaccc caacaataac ttacaggaag gcactgatcc taaaactgaa gaccccaacc 1140
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 cagcatggct tgcgttcaag actttctttt cctctttctt tccagaaggc ccccccagcc 1260
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 atactctatg tagttataa agcactgtac gtagaaggcc tttaggtgttgc catgtctatg 1560
 cttaggaaac tttccaaat gtgtgtgtct gcatgtgtgt ttgtacatag aagtcataga 1620
 tgagaaggta gttctgctgg tacgatttga ttccctgttgg aatgtttaaa ttacactaag 1680
 tgtactactt tatataatca atgaaattgc tagacatgtt tttagcaggac ttttcttagga 1740
 aagacttatg tataattgtt tttaaaatg cagtgtttt ctttaaacta agggaaactt 1800
 tgcggaggta aaaacctttt ctgggtttt tttcaataa agtttacta tgaatgaccc 1860
 taaaaaaaaaaaaaaa aaaaaaaa 1884

<210> 61
<211> 232
<212> PRT
<213> Homo sapiens

<400> 61
 Met Glu Ser Glu Thr Glu Pro Glu Pro Val Thr Leu Leu Val Lys Ser
 1 5 10 15
 Pro Asn Gln Arg His Arg Asp Leu Glu Leu Ser Gly Asp Arg Gly Trp
 20 25 30
 Ser Val Gly His Leu Lys Ala His Leu Ser Arg Val Tyr Pro Glu Arg
 35 40 45
 Pro Arg Pro Glu Asp Gln Arg Leu Ile Tyr Ser Gly Lys Leu Leu Leu
 50 55 60
 Asp His Gln Cys Leu Arg Asp Leu Leu Pro Lys Glu Lys Arg His Val
 65 70 75 80
 Leu His Leu Val Cys Asn Val Lys Ser Pro Ser Lys Met Pro Glu Ile
 85 90 95
 Asn Ala Lys Val Ala Glu Ser Thr Glu Glu Pro Ala Gly Ser Asn Arg
 100 105 110
 Gly Gln Tyr Pro Glu Asp Ser Ser Asp Gly Leu Arg Gln Arg Glu
 115 120 125
 Val Leu Arg Asn Leu Ser Ser Pro Gly Trp Glu Asn Ile Ser Arg His
 130 135 140
 His Val Gly Trp Phe Pro Phe Arg Pro Arg Pro Val Gln Asn Phe Pro
 145 150 155 160
 Asn Asp Gly Pro Pro Asp Val Val Asn Gln Asp Pro Asn Asn Asn
 165 170 175
 Leu Gln Glu Gly Thr Asp Pro Glu Thr Glu Asp Pro Asn His Leu Pro
 180 185 190
 Pro Asp Arg Asp Val Leu Asp Gly Glu Gln Thr Ser Pro Ser Phe Met
 195 200 205
 Ser Thr Ala Trp Leu Val Phe Lys Thr Phe Phe Ala Ser Leu Leu Pro
 210 215 220
 Glu Gly Pro Pro Ala Ile Ala Asn
 225 230

<210> 62
<211> 209
<212> PRT
<213> Homo sapiens

<400> 62
 Met Gln Tyr Leu Ala Ala Thr Ala Ala Ser Gly Ala Phe Val Pro Pro
 1 5 10 15
 Pro Ser Ala Gln Glu Ile Pro Val Val Ser Ala Pro Ala Pro Ala Pro
 20 25 30
 Ile His Asn Gln Phe Pro Ala Glu Asn Gln Pro Ala Asn Gln Asn Ala
 35 40 45

<210> 63
<211> 356
<212> PRT
<213> *Homo sapiens*

<400> 63
 Gly His Leu Lys Ala His Leu Ser Arg Val Tyr Pro Glu Arg Pro Arg
 1 5 10 15
 Pro Glu Asp Gln Arg Leu Ile Tyr Ser Gly Lys Leu Leu Leu Asp His
 20 25 30
 Gln Cys Leu Arg Asp Leu Leu Pro Lys Glu Lys Arg His Val Leu His
 35 40 45
 Leu Val Cys Asn Val Lys Ser Pro Ser Lys Met Pro Glu Ile Asn Ala
 50 55 60
 Lys Val Ala Glu Ser Thr Glu Glu Pro Ala Gly Ser Asn Arg Gly Gln
 65 70 75 80
 Tyr Pro Glu Asp Ser Ser Ser Asp Gly Leu Arg Gln Arg Glu Val Leu
 85 90 95
 Arg Asn Leu Ser Ser Pro Gly Trp Glu Asn Ile Ser Arg Pro Glu Ala
 100 105 110
 Ala Gln Gln Ala Phe Gln Gly Leu Gly Pro Gly Phe Ser Gly Tyr Thr
 115 120 125
 Pro Tyr Gly Trp Leu Gln Leu Ser Trp Phe Gln Gln Ile Tyr Ala Arg
 130 135 140
 Gln Tyr Tyr Met Gln Tyr Leu Ala Ala Thr Ala Ala Ser Gly Ala Phe
 145 150 155 160
 Val Pro Pro Pro Ser Ala Gln Glu Ile Pro Val Val Ser Ala Pro Ala
 165 170 175
 Pro Ala Pro Ile His Asn Gln Phe Pro Ala Glu Asn Gln Pro Ala Asn
 180 185 190
 Gln Asn Ala Ala Pro Gln Val Val Val Asn Pro Gly Ala Asn Gln Asn
 195 200 205
 Leu Arg Met Asn Ala Gln Gly Gly Pro Ile Val Glu Glu Asp Asp Glu
 210 215 220

Ile Asn Arg Asp Trp Leu Asp Trp Thr Tyr Ser Ala Ala Thr Phe Ser
 225 230 235 240
 Val Phe Leu Ser Ile Leu Tyr Phe Tyr Ser Ser Leu Ser Arg Phe Leu
 245 250 255
 Met Val Met Gly Ala Thr Val Val Met Tyr Leu His His Val Gly Trp
 260 265 270
 Phe Pro Phe Arg Pro Arg Pro Val Gln Asn Phe Pro Asn Asp Gly Pro
 275 280 285
 Pro Pro Asp Val Val Asn Gln Asp Pro Asn Asn Asn Leu Gln Glu Gly
 290 295 300
 Thr Asp Pro Glu Thr Glu Asp Pro Asn His Leu Pro Pro Asp Arg Asp
 305 310 315 320
 Val Leu Asp Gly Glu Gln Thr Ser Pro Ser Phe Met Ser Thr Ala Trp
 325 330 335
 Leu Val Phe Lys Thr Phe Phe Ala Ser Leu Leu Pro Glu Gly Pro Pro
 340 345 350
 Ala Ile Ala Asn
 355

<210> 64
<211> 391
<212> PRT
<213> Homo sapiens

<400> 64
 Met Glu Ser Glu Thr Glu Pro Glu Pro Val Thr Leu Leu Val Lys Ser
 1 5 10 15
 Pro Asn Gln Arg His Arg Asp Leu Glu Leu Ser Gly Asp Arg Gly Trp
 20 25 30
 Ser Val Gly His Leu Lys Ala His Leu Ser Arg Val Tyr Pro Glu Arg
 35 40 45
 Pro Arg Pro Glu Asp Gln Arg Leu Ile Tyr Ser Gly Lys Leu Leu Leu
 50 55 60
 Asp His Gln Cys Leu Arg Asp Leu Leu Pro Lys Gln Glu Lys Arg His
 65 70 75 80
 Val Leu His Leu Val Cys Asn Val Lys Ser Pro Ser Lys Met Pro Glu
 85 90 95
 Ile Asn Ala Lys Val Ala Glu Ser Thr Glu Glu Pro Ala Gly Ser Asn
 100 105 110
 Arg Gly Gln Tyr Pro Glu Asp Ser Ser Asp Gly Leu Arg Gln Arg
 115 120 125
 Glu Val Leu Arg Asn Leu Ser Ser Pro Gly Trp Glu Asn Ile Ser Arg
 130 135 140
 Pro Glu Ala Ala Gln Gln Ala Phe Gln Gly Leu Gly Pro Gly Phe Ser
 145 150 155 160
 Gly Tyr Thr Pro Tyr Gly Trp Leu Gln Leu Ser Trp Phe Gln Gln Ile
 165 170 175
 Tyr Ala Arg Gln Tyr Tyr Met Gln Tyr Leu Ala Ala Thr Ala Ala Ser
 180 185 190
 Gly Ala Phe Val Pro Pro Ser Ala Gln Glu Ile Pro Val Val Ser
 195 200 205
 Ala Pro Ala Pro Ala Pro Ile His Asn Gln Phe Pro Ala Glu Asn Gln
 210 215 220
 Pro Ala Asn Gln Asn Ala Ala Pro Gln Val Val Val Asn Pro Gly Ala
 225 230 235 240
 Asn Gln Asn Leu Arg Met Asn Ala Gln Gly Gly Pro Ile Val Glu Glu
 245 250 255

Asp	Asp	Glu	Ile	Asn	Arg	Asp	Trp	Leu	Asp	Trp	Thr	Tyr	Ser	Ala	Ala
			260				265								270
Thr	Phe	Ser	Val	Phe	Leu	Ser	Ile	Leu	Tyr	Phe	Tyr	Ser	Ser	Leu	Ser
			275				280								285
Arg	Phe	Leu	Met	Val	Met	Gly	Ala	Thr	Val	Val	Met	Tyr	Leu	His	His
			290			295					300				
Val	Gly	Trp	Phe	Pro	Phe	Arg	Pro	Arg	Pro	Val	Gln	Asn	Phe	Pro	Asn
			305			310				315					320
Asp	Gly	Pro	Pro	Asp	Val	Val	Asn	Gln	Asp	Pro	Asn	Asn	Asn	Leu	
			325			330									335
Gln	Glu	Gly	Thr	Asp	Pro	Glu	Thr	Glu	Asp	Pro	Asn	His	Leu	Pro	Pro
			340			345									350
Asp	Arg	Asp	Val	Leu	Asp	Gly	Glu	Gln	Thr	Ser	Pro	Ser	Phe	Met	Ser
			355			360							365		
Thr	Ala	Trp	Leu	Val	Phe	Lys	Thr	Phe	Phe	Ala	Ser	Leu	Leu	Pro	Glu
			370			375									380
Gly	Pro	Pro	Ala	Ile	Ala	Asn									
			385			390									

<210> 65
<211> 1857
<212> DNA
<213> Rat

<400> 65
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tgagcgcagt cgaggctcca ggcgcgcaga catggagccc gagccacagc ccgagccgg 120
cacgctgctg gtgaagagcc ccaatcagcg ccaccgcac ttggagctga gtggcgaccg 180
cggttggagt gtgagtcgcc tcaaggccca cctgagccga gtctaccccg aacgcccgcg 240
cccaaggaggac cagaggtaa tttattctgg gaagctgctg ttggatcacc aatgtctcca 300
agacttgctt ccaaaggcagg aaaaggcaca tggttgcac ctcgtgtca atgtgaggag 360
tccctcaaaa aagccagaag ccagcacaag gggtgctgag tccacagagc agccggacaa 420
caactagtcag gcacagtatc ctggggattc ctcaagcgat ggcttacggg aaagggaaatg 480
ccttcggAAC cttcctccct ctggatggga gaacgtctct aggccctgaag ccgtccagca 540
gactttccaa ggcctcgggc cccgcttctc tggctacacc acctacgggt ggctgcagct 600
ctcctgggtt cagcagatct atgcaagaca gtactacatg caatacttgg ctgccactgc 660
tgcttcagga gctttggcc ctacaccaag tgcacaagaa atacctgtgg tctctacacc 720
ggctcccgcc cctatacaca accagttcc ggcagaaaac cagccggcca atcagaatgc 780
agccgctcaa gcgggttta atcccgagc caatcagaac ttgcggatga atgcacaagg 840
cgccctctg gtgaaagaag atgatgagat aaaccgagac tgggtggatt ggacctactc 900
agcagcgaca tttccgttt tcctcagcat tcttacttc tactcctccc tgagcagatt 960
cctcatggtc atggcgcca ccgtagtcgt gtacctgcac cacgtcggtt gggttccatt 1020
cagacagagg ccagttcaga acttcccaga tgacggtccc ctcaggaag ctgccaacca 1080
ggaccccaac aataacctcc agggaggattt ggaccctgaa atggaagacc ccaaccgcct 1140
ccccgttaggc cgtgaagtgc tggaccctga gcataccagc ccctcggtca tgagcacagc 1200
atggctagtc ttcaagactt tctttgcctc tcttcttccg gaaggccccac cagcccttagc 1260
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ctggcgtgga ctcgagagag tcattgaaaaa cccacaggat gacgatgtgc ttctgtgcca 1380
agaaaagca caaactaaga catgaagccg tggtacaaac tgaacagggc ccctcatgtc 1440
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gcccgagggtc gcatgttctg cctgagcacc tccccagacg tttgtgcatt tttgtccgtac 1560
atgaaagtca tagacgtgtg tgcattgtgt ctctacatgg aagtcataga tgcagaaacg 1620
gttctgtgtt ttcgatttga ttccctgttgg aatgttgcattt tttactactt tttactactt 1680
tatataatca gtgacttgc agacatgttta gcaggacttt tcttaggagag acttattgtt 1740
tcattgtttt taaaacgcgtt gtcattttttt actgaggccg gcgacttggc acaggtaaag 1800
ccttgcgg gttttctgtt caataaaatgtt ttgttatgaa cgacaaaaaaa aaaaaaaaaa 1857

<210> 66

<211> 391
<212> PRT
<213> Rat

<400> 66
Met Glu Pro Glu Pro Gln Pro Glu Pro Val Thr Leu Leu Val Lys Ser
1 5 10 15
Pro Asn Gln Arg His Arg Asp Leu Glu Leu Ser Gly Asp Arg Gly Trp
20 25 30
Ser Val Ser Arg Leu Lys Ala His Leu Ser Arg Val Tyr Pro Glu Arg
35 40 45
Pro Arg Pro Glu Asp Gln Arg Leu Ile Tyr Ser Gly Lys Leu Leu Leu
50 55 60
Asp His Gln Cys Leu Gln Asp Leu Leu Pro Lys Gln Glu Lys Arg His
65 70 75 80
Val Leu His Leu Val Cys Asn Val Arg Ser Pro Ser Lys Lys Pro Glu
85 90 95
Ala Ser Thr Lys Gly Ala Glu Ser Thr Glu Gln Pro Asp Asn Thr Ser
100 105 110
Gln Ala Gln Tyr Pro Gly Asp Ser Ser Ser Asp Gly Leu Arg Glu Arg
115 120 125
Glu Val Leu Arg Asn Leu Pro Pro Ser Gly Trp Glu Asn Val Ser Arg
130 135 140
Pro Glu Ala Val Gln Gln Thr Phe Gln Gly Leu Gly Pro Gly Phe Ser
145 150 155 160
Gly Tyr Thr Thr Tyr Gly Trp Leu Gln Leu Ser Trp Phe Gln Gln Ile
165 170 175
Tyr Ala Arg Gln Tyr Tyr Met Gln Tyr Leu Ala Ala Thr Ala Ala Ser
180 185 190
Gly Ala Phe Gly Pro Thr Pro Ser Ala Gln Glu Ile Pro Val Val Ser
195 200 205
Thr Pro Ala Pro Ala Pro Ile His Asn Gln Phe Pro Ala Glu Asn Gln
210 215 220
Pro Ala Asn Gln Asn Ala Ala Ala Gln Ala Val Val Asn Pro Gly Ala
225 230 235 240
Asn Gln Asn Leu Arg Met Asn Ala Gln Gly Gly Pro Leu Val Glu Glu
245 250 255
Asp Asp Glu Ile Asn Arg Asp Trp Leu Asp Trp Thr Tyr Ser Ala Ala
260 265 270
Thr Phe Ser Val Phe Leu Ser Ile Leu Tyr Phe Tyr Ser Ser Leu Ser
275 280 285
Arg Phe Leu Met Val Met Gly Ala Thr Val Val Met Tyr Leu His His
290 295 300
Val Gly Trp Phe Pro Phe Arg Gln Arg Pro Val Gln Asn Phe Pro Asp
305 310 315 320
Asp Gly Pro Pro Gln Glu Ala Ala Asn Gln Asp Pro Asn Asn Asn Leu
325 330 335
Gln Gly Gly Leu Asp Pro Glu Met Glu Asp Pro Asn Arg Leu Pro Val
340 345 350
Gly Arg Glu Val Leu Asp Pro Glu His Thr Ser Pro Ser Phe Met Ser
355 360 365
Thr Ala Trp Leu Val Phe Lys Thr Phe Phe Ala Ser Leu Leu Pro Glu
370 375 380
Gly Pro Pro Ala Leu Ala Asn
385 390

<210> 67
<211> 1871

<212> DNA
 <213> Mouse

<400> 67
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 ctgagcgcag tcgagccgc acgcacgcg acatggagcc cgagccacag cccgagccgg 120
 tcacgctgct ggtgaagagt cccaatcagc gccaccgcga cttggagctg agtggcgacc 180
 gcagttggag tgtgagtcgc ctcaaggccc acctgagccg agtctacccc gagcgcggc 240
 gtccagagga ccagaggtta atttattctg ggaagctgct gttggatcac cagtgtctcc 300
 aagatttgct tccaaagcag gaaaagcgcac atgtttgca cttgtgtgc aatgtgaaga 360
 atccctccaa aatgccagaa accagcacaa agggtgctga atccacagag cagccggaca 420
 actctaataca gacacagcat cctggggact cctcaagtga tggttacgg caaagagaag 480
 ttcttcggaa cctttctccc tccggatggg agaacatctc taggccttag gctgtccagc 540
 agactttcca aggcctgggg cctggcttct ctggctacac aacgtatggg tggctgcagc 600
 tctcctgggtt ccagcagatc tatgcaaggc agtactacat gcaataactta gctgccactg 660
 ctgcatcagg aactttgtc cgcacaccaa gtgcacaaga gatacctgtg gtctctacac 720
 ctgctccggc tcctatacac aaccagttc cggcagaaaa ccagccggcc aatcagaatg 780
 cagctgctca agcggttgc aatccccgg ccaatcagaa cttgcggatg aatgcacaag 840
 gtggccccc ggtggaggaa gatgatgaga taaaccgaga ctgggttggat tggacctatt 900
 ccgcagcgcac gttttctgtt ttccctcagca tccttactt ctactcctcg ctgagcagat 960
 ttctcatggt catgggtgcc actgttagtca tgtacctgca ccacgtcggg tggttccgt 1020
 tcagacagag gccagttcag aacttcccgg atgatggtgg tcctcgagat gctgccaacc 1080
 aggaccccaa caataacctc cagggaggtt tggacccaga aatggaagac cccaaaccgccc 1140
 tccccccaga ccgcgaagtg ctggaccctg agcacaccag cccctcggtt atgagcacag 1200
 catggctagt cttcaagact ttctttgcct ctcttcttcc agaaggccca ccagccctag 1260
 ccaactgatg gcccctgtgc tctgtcgctg gtggcttga cagctcgac tggatcgtct 1320
 ggctccggct cctttccctc ccctggcgctg gactcgacag agtcattgaa aaccacagg 1380
 atgacatgtt cttctgtgcc aagaaaagc acaaactaag acatgaagcc gtggtacaaa 1440
 ctgaacaggg cccctcatgt cggttattctg aagagctta atgtataactg tatgtagtt 1500
 catagggact gtaagcagaa ggcccagggt cgcatgttct gcctgagcac ctcggat 1560
 gtgtgtgtcat gtgtgtgtta catggaaatgc atagacgtgt gtgcattgtt gctctacatg 1620
 gaagtcatag atgcagaaac gttctgtctg gttcgattt attcctgttg gaatgttcaa 1680
 attacactaa gtgtactact ttatataatc agtgaattgc tagacatgtt agcaggactt 1740
 ttcttaggaga gacttatgtta taattgtttt taaaatgca gtgccttct taaaaccgag 1800
 ggtggcgact tggcagaggtt aaaacctttt ccgagtttc tggcaataa agtttgcta 1860
 tgaatgactg t 1871

<210> 68
 <211> 391
 <212> PRT
 <213> Mouse

<400> 68
 Met Glu Pro Glu Pro Gln Pro Glu Pro Val Thr Leu Leu Val Lys Ser
 1 5 10 15
 Pro Asn Gln Arg His Arg Asp Leu Glu Leu Ser Gly Asp Arg Ser Trp
 20 25 30
 Ser Val Ser Arg Leu Lys Ala His Leu Ser Arg Val Tyr Pro Glu Arg
 35 40 45
 Pro Arg Pro Glu Asp Gln Arg Leu Ile Tyr Ser Gly Lys Leu Leu Leu
 50 55 60
 Asp His Gln Cys Leu Gln Asp Leu Leu Pro Lys Gln Glu Lys Arg His
 65 70 75 80
 Val Leu His Leu Val Cys Asn Val Lys Asn Pro Ser Lys Met Pro Glu
 85 90 95
 Thr Ser Thr Lys Gly Ala Glu Ser Thr Glu Gln Pro Asp Asn Ser Asn
 100 105 110
 Gln Thr Gln His Pro Gly Asp Ser Ser Ser Asp Gly Leu Arg Gln Arg
 115 120 125

Glu Val Leu Arg Asn Leu Ser Pro Ser Gly Trp Glu Asn Ile Ser Arg
 130 135 140
 Pro Glu Ala Val Gln Gln Thr Phe Gln Gly Leu Gly Pro Gly Phe Ser
 145 150 155 160
 Gly Tyr Thr Thr Tyr Gly Trp Leu Gln Leu Ser Trp Phe Gln Gln Ile
 165 170 175
 Tyr Ala Arg Gln Tyr Tyr Met Gln Tyr Leu Ala Ala Thr Ala Ala Ser
 180 185 190
 Gly Thr Phe Val Pro Thr Pro Ser Ala Gln Glu Ile Pro Val Val Ser
 195 200 205
 Thr Pro Ala Pro Ala Pro Ile His Asn Gln Phe Pro Ala Glu Asn Gln
 210 215 220
 Pro Ala Asn Gln Asn Ala Ala Gln Ala Val Val Asn Pro Gly Ala
 225 230 235 240
 Asn Gln Asn Leu Arg Met Asn Ala Gln Gly Gly Pro Leu Val Glu Glu
 245 250 255
 Asp Asp Glu Ile Asn Arg Asp Trp Leu Asp Trp Thr Tyr Ser Ala Ala
 260 265 270
 Thr Phe Ser Val Phe Leu Ser Ile Leu Tyr Phe Tyr Ser Ser Leu Ser
 275 280 285
 Arg Phe Leu Met Val Met Gly Ala Thr Val Val Met Tyr Leu His His
 290 295 300
 Val Gly Trp Phe Pro Phe Arg Gln Arg Pro Val Gln Asn Phe Pro Asp
 305 310 315 320
 Asp Gly Gly Pro Arg Asp Ala Ala Asn Gln Asp Pro Asn Asn Asn Leu
 325 330 335
 Gln Gly Gly Met Asp Pro Glu Met Glu Asp Pro Asn Arg Leu Pro Pro
 340 345 350
 Asp Arg Glu Val Leu Asp Pro Glu His Thr Ser Pro Ser Phe Met Ser
 355 360 365
 Thr Ala Trp Leu Val Phe Lys Thr Phe Phe Ala Ser Leu Leu Pro Glu
 370 375 380
 Gly Pro Pro Ala Leu Ala Asn
 385 390

<210> 69
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> siRNA

<400> 69
 gggaauguucu ucggaaccut t

21

<210> 70
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> siRNA

<400> 70
 ttcccucaa gaagccuugg a

21